

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L. et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSEE: Dr. Kathleen L. Horwath
  - (B) STREET: Department of Biological Sciences, Binghamton University
  - (C) CITY: Binghamton
  - (D) STATE: New York
  - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
  - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
  - (B) COMPUTER: IBM AT/ATX compatible
  - (C) OPERATING SYSTEM: Windows 95/98
  - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
  - (A) APPLICATION NUMBER: 60210446
  - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
  - (A) NAME: Mark Levy, Attorney-at-Law
  - (B) REGISTRATION NUMBER: 29,188
  - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
  - (A) TELEPHONE: 607-722-6600
  - (B) TELEFAX: 607-724-2207

09876796-060701

## (2) INFORMATION FOR SEQ. ID NO: 1

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(ix) FEATURES:

(D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val
1				5					10					15				

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## (2) INFORMATION FOR SEQ. ID NO: 2

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, signal plus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC	36
Met Lys Leu Leu	-15
TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG	81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu	1
	-10 -5
ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT	126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys	5 10 15
CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC	171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg	20 25 30
AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT	216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe	35 40 45
TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG	261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val	50 55 60
GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC	306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn	65 70 75
GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA	351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg	80 85 90
GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG	396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met	95 100 105
AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA	439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *	110 115
CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAT AAAGTGTTC	489
TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG	539
CGGCCGCGGG CCCATCGTTT TCCACCC	566

## (2) INFORMATION FOR SEQ. ID NO: 3

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 13.17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val  
 -15 -10 -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys  
 1 5 10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala  
 15 20 25 30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe  
 35 40 45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val  
 50 55 60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu  
 65 70 75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val  
 80 85 90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro  
 95 100 105 110

Lys Phe Ser Pro Val Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 4

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 13.17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys  
 1 5 10 15  
 Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn  
 20 25 30  
 Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val  
 35 40 45  
 Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp  
 50 55 60  
 Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr  
 65 70 75 80  
 Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu  
 85 90 95  
 Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe  
 100 105 110  
 Ser Pro Val Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTGTGTA TTTGACTGAA TTTTGACAAT AAAGGTAATA 455  
 Ile Asp \*  
 115

TCGTTATGTA AAAAAAAAAA AAAAAA 481

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- (2) INFORMATION FOR SEQ. ID NO: 6
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.3
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTGTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 455  
 Ile Asp \*  
 115

TCGTTATGAA AAAAAAAAAA AAAAAAA 482

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## (2) INFORMATION FOR SEQ. ID NO: 7

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
 95 100 105 110

Phe Ser Pro Ile Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 8

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 12.84

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
 1 5 10 15  
 Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
 20 25 30  
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
 35 40 45  
 Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
 50 55 60  
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
 65 70 75 80  
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
 85 90 95  
 Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110  
 Pro Ile Asp \*  
 115

## (2) INFORMATION FOR SEQ. ID NO: 9

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 455  
 Ile Asp \*  
 115

TCGTTATGTA AAAAAAAAAA AAAAAA 481

0926796-060701

## (2) INFORMATION FOR SEQ. ID NO: 10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Clone 3.4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp  
 95 100 105 110

Phe Ser Pro Ile Asp \*  
 115

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## (2) INFORMATION FOR SEQ. ID NO: 11

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Clone 3.4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
 1 5 10 15  
 Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
 20 25 30  
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
 35 40 45  
 Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
 50 55 60  
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
 65 70 75 80  
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
 85 90 95  
 Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110  
 Pro Ile Asp \*  
 115

09876796-060701

## (2) INFORMATION FOR SEQ. ID NO: 12

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC 46  
 Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTGTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 455  
 Ile Asp \*  
 115

TCGTTATGAA AAAAAAAAAA AAAAAAAAAA 482

09876543210

## (2) INFORMATION FOR SEQ. ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

## (2) INFORMATION FOR SEQ. ID NO: 14

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature protein for Clone 3.9

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
 1 5 10 15  
 Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
 20 25 30  
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
 35 40 45  
 Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
 50 55 60  
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
 65 70 75 80  
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
 85 90 95  
 Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110  
 Pro Ile Asp \*  
 115

09876796-060701

## (2) INFORMATION FOR SEQ. ID NO: 15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC 46  
 Met Lys Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA 90  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTGTGTA TTTGGCTGAA TTTTGACAAT AAAGGTACTA 455  
 Ile Asp \*  
 115

TCGTTATGTA AAAAAAAAAA AAAAAA 481

09876796-060701



## (2) INFORMATION FOR SEQ. ID NO: 16

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus

098796-060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

## (2) INFORMATION FOR SEQ. ID NO: 18

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186  
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
-5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231  
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT 276  
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321  
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr  
40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366  
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys  
55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411  
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile  
70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456  
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543  
Pro Ile Asp \*  
115

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 20
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 682 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.3
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal Plus

09876796-050701

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-55 -50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-45 -40 -35

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met  
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT 231  
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276  
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser  
1 5 10

AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321  
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp  
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG 366  
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys  
30 35 40

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC 411  
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala  
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456  
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val  
60 65 70

GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501  
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val  
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT 546  
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys  
90 95 100

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA 595  
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA 645

AAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT 682

090716795-060704

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(B) CLONE: 2.3

(D) OTHER INFORMATION: Precursor Protein with His-tag

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115



- (2) INFORMATION FOR SEQ. ID NO: 22
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 543 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.3
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal minus
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
          -15                       -10                       -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 24
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 777 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 13.17
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal plus

09876543210-060704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-65 -60 -55

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-50 -45 -40

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile  
-35 -30 -25

CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC 231  
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser  
-20 -15 -10

CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT 276  
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile  
-5 1 5

GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA 321  
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly  
10 15 20

GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG 366  
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu  
25 30 35

GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC 411  
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn  
40 45 50

GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG 456  
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu  
55 60 65

AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG 501  
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu  
70 75 80

AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG 546  
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu  
85 90 95

ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG 595  
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys  
100 105 110

TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG 643  
Phe Ser Pro Val Asp \*  
115

TGTGCTTTAC ATATAAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA 693

AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT 743

TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT 777

T02090" 96/9/86

## (2) INFORMATION FOR SEQ. ID NO: 25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile  
 -25 -20 -15 -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile  
 -5 1 5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val  
 10 15 20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp  
 25 30 35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu  
 40 45 50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val  
 55 60 65 70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys  
 75 80 85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe  
 90 95 100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp \*  
 105 110 115

F02090"96292860

## (2) INFORMATION FOR SEQ. ID NO: 26

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

## (2) INFORMATION FOR SEQ. ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys  
1 5 10 15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg  
20 25 30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys  
35 40 45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val  
50 55 60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu  
65 70 75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu  
80 85 90 95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys  
100 105 110

Phe Ser Pro Val Asp \*  
115

## (2) INFORMATION FOR SEQ. ID NO: 28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*  
(B) INDIVIDUAL/ISOLATE: none  
(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA  
(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal plus



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-55 -50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-45 -40 -35

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met  
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT 231  
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276  
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser  
1 5 10

AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321  
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp  
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG 366  
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys  
30 35 40

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC 411  
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala  
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456  
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val  
60 65 70

GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501  
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val  
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT 546  
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val  
90 95 100

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA 595  
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA 645

AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT 681

09876543210

## (2) INFORMATION FOR SEQ. ID NO: 29

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Precursor protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
 90 95 100

Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
 105 110 115

F02090"967960

- (2) INFORMATION FOR SEQ. ID NO: 30
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
  - (B) CLONE: 3.4
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186  
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
-5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231  
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276  
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321  
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr  
40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366  
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys  
55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411  
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile  
70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 456  
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
85 90 95

TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT 543  
Pro Ile Asp \*  
115

## (2) INFORMATION FOR SEQ. ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

```
(iv) ANTI-SENSE: no
```

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

- (2) INFORMATION FOR SEQ. ID NO: 32
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 682 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 3.9
  - (ix) FEATURES
    - (D) OTHER INFORMATION: His-tagged, Signal plus

09876796-060701

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-55 -50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-45 -40 -35

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met  
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT 231  
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276  
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser  
1 5 10

AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321  
Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp  
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG 366  
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys  
30 35 40

CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC 411  
His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala  
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456  
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val  
60 65 70

GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501  
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val  
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT 546  
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys  
90 95 100

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA 595  
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA 645

AAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT 682

T02090 96796 060701

## (2) INFORMATION FOR SEQ. ID NO: 33

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

## (ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val  
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val  
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
 55 60 65 70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
 105 110 115

050706-050701

(i) SEQUENCE CHARACTERISTICS:

- |                 |                 |                     |                     |            |     |
|-----------------|-----------------|---------------------|---------------------|------------|-----|
| TTGTTAGCGG      | ATGGAATTCC      | CTCGTAGGGG          | ATAATTTTGT          | TTACTTTAAG | 50  |
| AAGGAGATAT      | ACC             | ATG GGC AGC AGC     | CAT CAT CAT CAT CAT | CAC AGC    | 96  |
|                 | Met Gly Ser Ser | His His His His His |                     | His Ser    |     |
|                 |                 | -30                 |                     | -25        |     |
| AGC GGC CTG GTG | CCG CGC GGC AGC | CAT ATG GCT AGC     | ATG ACT GGT         |            | 141 |
| Ser Gly Leu Val | Pro Arg Gly Ser | His Met Ala Ser     | Met Thr Gly         |            |     |
|                 | -20             | -15                 | -10                 |            |     |
| GGA CAG CAA ATG | GGT CGC GGA TCC | CTC ACC GAT GAA     | CAG ATA CAG         |            | 186 |
| Gly Gln Gln Met | Gly Arg Gly Ser | Leu Thr Asp Glu     | Gln Ile Gln         |            |     |
|                 | -5              | 1                   | 5                   |            |     |
| AAA AGG AAC AAG | ATC AGC AAA GAA | TGC CAG CAG GAG     | TCC GGA GTG         |            | 231 |
| Lys Arg Asn Lys | Ile Ser Lys Glu | Cys Gln Gln Glu     | Ser Gly Val         |            |     |
|                 | 10              | 15                  | 20                  |            |     |
| TCC CAA GAG ACG | ATC GAC AAA GTC | CGC ACA GGT GTC     | TTG GTC GAC         |            | 276 |
| Ser Gln Glu Thr | Ile Asp Lys Val | Arg Thr Gly Val     | Leu Val Asp         |            |     |
|                 | 25              | 30                  | 35                  |            |     |
| GAT CCC AAA ATG | AAG AAG CAC GTC | CTC TGC TTC TCG     | AAG AGA ACT         |            | 321 |
| Asp Pro Lys Met | Lys Lys His Val | Leu Cys Phe Ser     | Lys Arg Thr         |            |     |
|                 | 40              | 45                  | 50                  |            |     |
| GGA GTG GCA ACC | GAA GCC GGA GAC | ACC AAT GTG GAG     | GTA CTC AAA         |            | 366 |
| Gly Val Ala Thr | Glu Ala Gly Asp | Thr Asn Val Glu     | Val Leu Lys         |            |     |
|                 | 55              | 60                  | 65                  |            |     |
| GCC AAG CTG AAG | CAT GTG GCC AGC | GAC GAA GAA GTG     | GAC AAG ATC         |            | 411 |
| Ala Lys Leu Lys | His Val Ala Ser | Asp Glu Glu Val     | Asp Lys Ile         |            |     |
|                 | 70              | 75                  | 80                  |            |     |
| GTG CAG AAG TGC | GTG GTC AAG AAG | GCC ACA CCA GAG     | GAA ACG GCT         |            | 456 |
| Val Gln Lys Cys | Val Val Lys Lys | Ala Thr Pro Glu     | Glu Thr Ala         |            |     |
|                 | 85              | 90                  | 95                  |            |     |
| TAT GAC ACC TTC | AAG TGT ATT TAC | GAC AGT AAA CCT     | GAT TTC TCT         |            | 501 |
| Tyr Asp Thr Phe | Lys Cys Ile Tyr | Asp Ser Lys Pro     | Asp Phe Ser         |            |     |
|                 | 100             | 105                 | 110                 |            |     |
| CCT ATT GAT TAA | CTCGAGCACC      | ACCACCACCA          | CCACTGAGAT          |            | 543 |
| Pro Ile Asp *   |                 |                     |                     |            |     |
|                 | 115             |                     |                     |            |     |



## (2) INFORMATION FOR SEQ. ID NO: 35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
                   -30                  -25                  -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
                   -15                  -10                  -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
                   1                  5                  10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
   15                  20                  25                  30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
                   35                  40                  45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
                   50                  55                  60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
                   65                  70                  75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
   80                  85                  90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
   95                  100                  105                  110

Phe Ser Pro Ile Asp \*  
                   115

T02090"96292860

## (2) INFORMATION FOR SEQ. ID NO: 36

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 681 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Tenebrio molitor
    (B) INDIVIDUAL/ISOLATE: none
    (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: cDNA
    (B) CLONE: 7.5
(ix) FEATURES
    (D) OTHER INFORMATION: His-tagged, Signal plus
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96  
Met Gly Ser Ser His His His His His His Ser  
-55 -50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
-45 -40 -35

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186  
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met  
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT 231  
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276  
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser  
1 5 10

AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321  
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp  
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG 366  
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys  
30 35 40

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC 411  
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala  
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456  
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val  
60 65 70

GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501  
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val  
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT 546  
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys  
90 95 100

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA 595  
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

TTTGGCTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAAA 645

AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT 681

09876543210

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(C) STRANDEDNESS: single

MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
105 110 115

## (2) INFORMATION FOR SEQ. ID NO: 38

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|                                                             |     |
|-------------------------------------------------------------|-----|
| TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG      | 50  |
| AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC  | 96  |
| Met Gly Ser Ser His His His His His His Ser                 |     |
| -30 -25                                                     |     |
| AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT | 141 |
| Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly |     |
| -20 -15 -10                                                 |     |
| GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG | 186 |
| Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln |     |
| -5 1 5                                                      |     |
| AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG | 231 |
| Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val |     |
| 10 15 20                                                    |     |
| TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC | 276 |
| Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp |     |
| 25 30 35                                                    |     |
| GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT | 321 |
| Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr |     |
| 40 45 50                                                    |     |
| GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA | 366 |
| Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys |     |
| 55 60 65                                                    |     |
| GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC | 411 |
| Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile |     |
| 70 75 80                                                    |     |
| GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT | 456 |
| Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala |     |
| 85 90 95                                                    |     |
| TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT | 501 |
| Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser |     |
| 100 105 110                                                 |     |
| CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT            | 543 |
| Pro Ile Asp *                                               |     |
| 115                                                         |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

HYPOTHETICAL: no

(vi) ORIGINAL SOURCE:

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*  
115

## (2) INFORMATION FOR SEQ. ID NO: 40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5

## (ix) FEATURES

- (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-H1 site

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG

24

09876795-060701

- (2) INFORMATION FOR SEQ. ID NO: 41
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

09876796-060701



## (2) INFORMATION FOR SEQ. ID NO: 42

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-HI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA

24

T02090 96796 060701

(2) INFORMATION FOR SEQ. ID NO: 43

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Tenebrio molitor
    (B) INDIVIDUAL/ISOLATE: none
    (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: cDNA
    (B) CLONE: 13.17
(ix) FEATURES
    (D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
```

GAGTGGTCAA CTAAGTGAGC TCGCC 25

0826907

- (2) INFORMATION FOR SEQ. ID NO: 44
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v)
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCN TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAY GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAR TGC CAG CAG GNG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAY GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG ARA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAR GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG NNT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTTGTA TTTGCTGAA TTTTGACAAT AAAGGTANTA	455
Ile Asp *	
115	
TCGTTATGNA AAAAAAAAAA AAAAAA	481

## (2) INFORMATION FOR SEQ. ID NO: 45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

## (ix) FEATURES

- (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GGCANRRNNNN	AAR	ATG	AAR	YTN	CTC	TNN	TGY	YTN	RYN	TYC	NYC	RYY		46	
	Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala				
						-15									
NTN	NTN	RTC	RNA	GYT	CAG	GCY	CTN	ACC	GAN	GNA	CAR	ATN	NAG	AAA	91
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	
			-5				1				5				
NNG	AAC	AAG	ATC	AGC	AAA	RAR	TGY	CAR	NAN	GNR	NNY	GGA	GTG	TCN	136
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	
	10					15					20				
CAA	GAG	AYN	ATN	RNC	AAA	GYT	CGC	ANN	GGT	GNC	TNG	GNN	GAY	GAT	181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	
	25					30					35				
CCY	AAA	NTG	AAR	NRN	CAN	GTY	YTY	TGC	NTN	NCN	ARG	ARN	RCY	GGN	226
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	
	40					45					50				
NTG	GCN	ACN	GAA	NCN	GGA	GAN	RYN	RNN	GTN	GAN	GTR	YTN	ARR	GNN	271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	
	55					60					65				
AAG	NTG	ARG	NAN	GTN	RCY	RRC	AAC	GAC	GAA	GAR	RYN	GAN	AAR	ATC	316
Lys	Leu	Lys	His	Val	Ala	Ser	Asn	Asp	Glu	Glu	Val	Asp	Lys	Ile	
	70					75					80				
RTN	NAN	AAG	TGC	GYN	GTC	AAG	ARR	GNY	ACN	NYN	GAR	GAR	ACG	GYN	361
Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	
	85					90					95				
TNY	RAY	ACY	TTC	AAR	NNT	RTY	NNN	RAN	ARY	AAR	CCN	RAN	TTC	TCN	406
Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	
	100					105					110				
CCN	RTT	GAT	TRA	NYNNYYNNNA	YTNGNNNRNR	NTTYRANAAT	AAAGNNNNNTN								458
Pro	Ile	Asp	*												
	115														
TNRTNNNRNA	AAAAAAAAAA	AAAAAA													484

- (2) INFORMATION FOR SEQ. ID NO: 46
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (iii) HYPOTHETICAL: no
  - (iv) ANTI-SENSE: no
  - (v)
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: *Tenebrio molitor*
    - (B) INDIVIDUAL/ISOLATE: none
    - (C) CELL TYPE: fat body and whole organism
  - (vii) IMMEDIATE SOURCE:
    - (A) LIBRARY: cDNA
    - (B) CLONE: 2.2
  - (ix) FEATURES
    - (D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYY NYC RYY	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
NTN NTN RTC NNA GYT CAG GCY NTN ACY NAN GNA NAN NTN NAG NNA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
NNG NNC NAR AYC AGC RNA RAR TGY NAR NNN GNR NNY GGA GTG TCN	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
NAA GAN RYN ATN RNN ARA GYY CGC ANN GGT GNC TNG GNN GAY GAY	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCY AAA NTG AAR NNN CAN NTY YTY TGC NTN NYN ARG RNN NYN GRN	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
NTR GYN RCN GAA NCN GGA GAN RYN RNN GYN GAN RYR YTN ARR GNN	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG NTG ANG NRN NNN NNN RNN ANN RNN RAR RAR RYN RRN ARR NTN	316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile	
70 75 80	
NYN NRN ARN NNN NNN NNN NNG ARN RNN NYN NNN RAR RNR NNN NNN	361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN CCN RNN TYY TYN	406
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CNN RYT RNT TRN NYNNNNNNNN YNNGNNNRNR NTTYRANAAT AAAGNNNYTN	458
Pro Ile Asp *	
115	
TNRTNNNRNA AAAAAAAAAA AAAAAA	484

(2) INFORMATION FOR SEQ. ID NO: 47

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGCNNRNNNN AAR ATG AAR YTN CTC YNN TGY YTN RYN YYY NY Y RYY 46  
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
-15 -10

NTN NTN RYC NNR RYY YAN GCY NTN ACY NAN RNA NNN NNN NAG NNR 91  
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
-5 1 5

NNG NNY NAR NNC AGC RNN RNN TGY NAR NNN GNR NNY GGA GTR TCN 136  
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser  
10 15 20

NAA GAN NYN NTN RNN ARR GYY CGC ANN NGT GNN NNR GNN GAY GAY 181  
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

CCY AAA NTG AAR NNN CAN NYY YTY TGC NTN NYN ARG RNN NYY GRN 226  
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
40 45 50

NTN RYN RNN GNN NNN GGN GAN NYN NNN NYN GAN NNN NTN ARR RNN 271  
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
55 60 65

AAR NTN ANG NRN NNN NNN RNN RNN NNN RAR RAR RYN RRN RRN NTN 316  
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile  
70 75 80

NYN NNN ARN NNN NNN NNN NNG ARN RNN NYN NNN NAR NNN NNN NNN 361  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
     85                    90                    95

NNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN YCN NNN TNN NNN 406  
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
100 105 110

CNN NYN RNN TRN NNNNNNNNNN YNNRNNNNNN NNNNNNNAAT AAANNNNNNNN 458  
Pro Ile Asp \*  
115

NNNNNNNNNA AAAAAAAAAA AAAAAA 484

[illegible]

(2) INFORMATION FOR SEQ. ID NO: 48

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 133 Amino Acids
    (B) TYPE: Amino Acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Protein
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Tenebrio molitor
    (B) INDIVIDUAL/ISOLATE: none
    (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
    (A) LIBRARY: cDNA
    (B) CLONE:
(ix) FEATURES
    (D) OTHER INFORMATION: Genral Consensus of Clones,
                           B1, B2 and AFP-3
```

[illegible]

RB125 SEQ